

FIG. 1A

1	CCCACGCGTCCGATTAAAGTGAGGAGAGAGCTACAAACCAAGTAAGCAAGTGTCAAGGGCTC	60
61	ACCAACCATGCAAGGGACAGGGCAGGAGAAGAGGAACCTGCAAAGACATATTTGTTCCAA	120
1	<u>M Q G Q G R R R G T C K D I F C S K</u>	18
121	AATGGCATCTTACCTTATGGAGTACTCTTGCTGTTGGCCTCTGTGCTCCAATCTACTG	180
19	<u>M A S Y L Y G V L F A V G L C A P I Y C</u>	38
181	TGTGTCCCCGGCCAATGCCCGACTGCAACACCGACTTTGCCTCCGCCTACCGCAGGGCTGGT	240
39	<u>V S P A N A P S A Y P R P S S T K S T P</u>	58
241	TGCCTCACAGGTGTATTCCCTCAACACCGACTTTGCCTCCGCCTACCGCAGGGCTGGT	300
59	<u>A S Q V Y S L N T D F A F R L Y R R L V</u>	78
301	TTTGGAGACCCCGAGTCAGAACATCTCTTCTCCCGTGTGAGTGTCTCCACCTCCCTGGC	360
79	<u>L E T P S Q N I F F S P V S V S T S L A</u>	98
361	CATGCTCTCCCTGGGCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGCTT	420
99	<u>M L S L G A H S V T K T Q I L Q G L G F</u>	118
421	CAACCTCACACACACACCAGAGTCTGCCATCCACCCAGGGCTTCCAGCACCTGGTTCACTC	480
119	<u>N L T H T P E S A I H Q G F Q H L V H S</u>	138
481	ACTGACTGTTCCAGCAAAGACCTGACCTTGAAGATGGAAAGTGCCCTTCGTCAAGAA	540
139	<u>L T V P S K D L T L K M G S A L F V K K</u>	158
541	GGAGCTGCAGCTGCAGGCAAATTCTGGCAATGTCAAGAGGCTGTATGAAGCAGAAAGT	600
159	<u>E L Q L Q A N F L G N V K R L Y E A E V</u>	178
601	CTTTTCTACAGATTCTCCAACCCCTCATTGCCAGGCGAGGATCAACAGCCATGTGAA	660
179	<u>F S T D F S N P S I A Q A R I N S H V K</u>	198
661	AAAGAAGACCCAAAGGGAGGTTGTAGACATAATCCAAGGCCTTGACCTCTGACGCCAT	720
199	<u>K K T Q G K V V D I I Q G L D L L T A M</u>	218
721	GGTTCTGGTGAATCACATTCTTAAAGCCAAGTGGAGAAGCCCTTCACCTTGAATA	780
219	<u>V L V N H I F F K A K W E K P F H L E Y</u>	238
781	TACAAGAAAGAACTTCCCATTCTGGTGGCGAGCAGGTCACTGTGCAAGTCCCCATGAT	840
239	<u>T R K N F P F L V G E Q V T V Q V P M M</u>	258
841	GCACCAGAAAGAGCAGTCGCTTGGGTGGATACAGAGCTGAACGTGCTTGTGCTGCA	900
259	<u>H Q K E Q F A F G V D T E L N C F V L Q</u>	278

FIG. 1B

901	GATGGATTACAAGGGAGATGCCGTGGCCTTCTTGTCCCTCCCTAGCAAGGGCAAGATGAG	960
279	M D Y K G D A V A F F V L P S K G K M R	298
961	GCAACTGGAACAGGCCTTGTCAGCCAGAACACTGATAAAAGTGGAGCCACTCACTCCAGAA	1020
299	Q L E Q A L S A R T L I K W S H S L Q K	318
1021	AAGGTGGATAGAGGTGTTCATCCCCAGATTTCCATTCTGCCCTACAAATCTGGAAAC	1080
319	R W I E V F I P R F S I S A S Y N L E T	338
1081	CATCCTCCCGAAGATGGGCATCCAAAATGCCCTTGACAAAAATGCTGATTTCTGGAAT	1140
339	I L P K M G I Q N A F D K N A D F S G I	358
1141	TGCAAAGAGAGACTCCCTGCAGGTTCTAAAGCAACCCACAAGGCTGTGCTGGATGTCAG	1200
359	A K R D S L Q V S K A T H K A V L D V S	378
1201	TGAAGAGGGCACTGAGGCCACAGCAGTACCAACCAAGTTCATAGTCCGATCGAAGGA	1260
379	E E G T E <u>A T A A T T T K F I V R S K D</u>	398
1261	TGGTCCCTCTTACTTCACTGTCTCCTTCAATAGGACCTTCTGATGATGATTACAATAA	1320
399	G P S Y F T <u>V S F N R T F L M M I T N K</u>	418
1321	AGCCACAGACGGTATTCTCTTCTAGGGAAAGTGGAAAATCCACTAAATCCTAGGTGGG	1380
419	A T D G I L F L G K V E N P T K S *	436
1381	AAATGGCCTGTTAACTGATGGCACATTGCTAATGCACAAGAAATAACAAACCACATCCCT	1440
1441	CTTTCTGTTCTGAGGGTGCATTGACCCAGTGGAGCTGGATTGCTGGCAGGGATGCCA	1500
1501	CTTCCAAGGCTCAATCACCAAAACCATCAACAGGGACCCAGTCACAAGCCAACACCCATT	1560
1561	AACCCCAAGTCAGTGCCCTTTCCACAAATTCTCCAGGTAACTAGCTTCAATGGATGTTG	1620
1621	CTGGGTTACCATATTCCATTCTGGGCTCCAGGAATGGAAATACGCCAACCCAGGT	1680
1681	TAGGCACCTCTATTGCAGAATTACAATAACACATTCAATAAAACTAAAATATGAAAAAAA	1740
1741	AAAAAAAAAAAAAAAAAAAAAAA 1766	

FIG. 2

AL132708_FL	1	50
AACT_HUMAN	(1) MQGQGRRRGTCDFCSKMASYLYGV EFAVCF APIYCVSPANAPSAYPR	
KAIN_HUMAN	(1) -----MERMLPE LA AGFCPAVLCHPNPLD	
THBG_HUMAN	(1) -----MHLIDYLL LLV ALSHGQLHVEHDGESCS	
	-----MSPFLYLV LLV LBHATIHCASPEGKVTACHS	
AL132708_FL	51	100
AACT_HUMAN	(51) PS-----STKSTPASQVYSLNTDFAFR LY YRRLVLET PSQNIFF SPVSV	
KAIN_HUMAN	(31) EENLTQENQDRGTHV D LG A SANV D FA RS LYKQLVLKA P DKN V IF SP LSI	
THBG_HUMAN	(33) NSSHQQILET G EGSP SL KIA P ANAD FA FR Y LI A SET PG KN I FF SP LSI	
	(33) -----SQPNATLYKMSSINAD FA ENLYYR RF T V ET P DKN I FF SP VSI	
AL132708_FL	101	150
AACT_HUMAN	(94) STSLAM I SLGAH S VTKTQ I LQGLGF N HTPESAIHQG F QH I VH S ETVPS	
KAIN_HUMAN	(81) STALAF I SLGAHNTT L T E ILKGLK N ET E TSEAEIHQS F QH I LRT E NQSS	
THBG_HUMAN	(83) SAAYAM I SLGACSHRSQ I LEGL G EN I TE L SESDVHRG F QH I LHT E N L PG	
	(74) SAALV M LSFGACC S TQ T E V ET L GEN I TD T PM V E I QHG F QH I IC S EN FP K	
AL132708_FL	151	200
AACT_HUMAN	(144) K E ETLKMGS A LFVKK E QLQ A NE L GNVKRL Y EA E VE S T E DSNPSIAQARI	
KAIN_HUMAN	(131) D E LQLSMGN A MFV K EQLS L DR F TE A KRL Y GSE A FA T D F QDSAAAKL I	
THBG_HUMAN	(133) H G LET R VGS A LE L SHN E KFLAKFLN D TM A V Y AKL E HTNFY D TVGT I QL I	
	(124) K E EELQ I GN A LF I GKHLKPLAK E LNDV K TL Y ET E VE S T E DSN I AAK Q E I	
AL132708_FL	201	250
AACT_HUMAN	(194) NSHVKKK I QGKVVD I IQG I DL L T A M V I V NH I FF K AKWEK P FHLEY F TRKNF	
KAIN_HUMAN	(181) NDY V KNG T RGK I TD L IKD E DSQTMM V I V NY I FF K AKWEK P FISSRT TP KD	
THBG_HUMAN	(183) NDHVKKETRGK I VDLV S E I KKDVL M V I V NY I FF K AKWEK P FISSRT TP KD	
	(174) NSHVEMQ T KGKVVG L IQD L KPNT I M V I V NY I HF K AQWANPF D PSKTEDSS	
AL132708_FL	251	300
AACT_HUMAN	(244) PFLVGEQVT V QVPM M HQ K EQFAFGV D TE I N C F V LQMD Y KGD A VAFF V IPS	
KAIN_HUMAN	(231) FYLSKKWVMVP M SLH H LT I PYFR D E B L S C T V E L K Y T GN A SA E IPD	
THBG_HUMAN	(233) FYVDENT T VRVP M MLQDQ E HHWYL H ERY L PC S VL R MD Y KGD A TV F E I PN	
	(224) SFLIDKTT T TVQVPM M HQ M EQYY H L V DEM E LN C V L QMD Y SKN A LA E VE P K	
AL132708_FL	301	350
AACT_HUMAN	(294) KGKMRQ L EQ A SART L IKWSH H SLQKR --- WIEVF I P R S ISAS Y NET I	
KAIN_HUMAN	(281) QDKMEE V EAM L L P ET L KR W R D S L E F R --- EIGELYLP K F S IS R D Y N L ND I	
THBG_HUMAN	(283) QGKMRE I E V L T PE M LMR W NN L R K R N F Y K K L E L H L P K F S IS G SY V LDQ I	
	(274) EGQMES V EA A MS S KT I KK W N R L E Q K G --- W V DL F V P K F S IS A T Y D G AT	
AL132708_FL	351	400
AACT_HUMAN	(340) E P KM G I Q NAFDKN A DFSGIAKRD S LO V SKATH K A V LD V SEEG T E A TA A TT	
KAIN_HUMAN	(328) E L QLG I EEAFT S KAD L SG I IT G ARN L AV S Q V V H K A V LD V FE E G T E A SA A TA	
THBG_HUMAN	(333) E P RLG F TD L FSK W AD L SG I IT K Q Q K L EA S K F H K A T LD V DE A G T E A AA A TT	
	(320) E L KM G I Q HAYSEN A DFSG L TE D NG I K L S N AA H K A V I HIG E K G TE A AA A V P E	
AL132708_FL	401	446
AACT_HUMAN	(390) TKFIVRSKDGPSYFT V S F N R T E L MM I T N K A T D G I L F LG K V E N P TK S	
KAIN_HUMAN	(378) VKITL L S A LV E TR T IV R FN R P E L M IT V P T D T Q N I F MS X V T N P K Q A	
THBG_HUMAN	(383) FAIKFFSAQTN - RHILRFN R P E L V V I F S T S T Q S V L FL G K V V D PT K P	
	(370) VELSDQ P ENT F L H PI I Q I D R S M L I ER S TR S I L FL G K V V N P T E A	

FIG. 3

LSI-01 pdb1qlp	MQGQGRRRG T CKDIFCSKMA SYLYGVLF A V GLCAPIYCVS P A N P S A Y P R MDPQ GDAQKTDTS
LSI-01 pdb1qlp	PSSTKSTPAS QVYSINTDPA F R I K R R R E V L E T P S Q M E R S P V S V S E S L A M E HHDQDHPTFN K I T P N L A E H A K S I Y R O H A Q S N S T M E R E S P V S I A M A F A M L
LSI-01 pdb1qlp	S I G A H S V E K T Q I E Q S E G I N L T H T P E S A T H Q G E C H I V H S E T V B S K D E T E K M S I G T K A D T H D E I E G E G E N F N L T E I P E A Q H E G E C E L L R T E N Q B D S Q E Q B T T
LSI-01 pdb1qlp	G S A I F V K K E L Q I Q A N E L G N V K R E V E A E V S T D E S N P S I A Q A R E N S H U K R K G N G E F L S E G L K E V D K M I E D V K E L V H S E A F T V N E G D T E E N K K Q I N D Y V E N G
LSI-01 pdb1qlp	T Q G K V V D I I Q G I D L L T A M V L V N B I G F F K A K W E K P F H L E Y T R K N F P E L V G E Q T Q G K I V D L V K E I D R D T V F A L V N Y I I P K G K W E R F E V K D T . E E E D E B V D Q V
LSI-01 pdb1qlp	V T V Q V P M M H Q K E Q F A F G V D T E I N C F V E Q M D Y K G D A V A F F V L P S K G K M R Q E T T V K V P M M K R L G M F N I Q H C K K I S S W W E L M K Y L G N A T A I F F E P D E G K L Q H I
LSI-01 pdb1qlp	E Q A I S A R T L I K W S H S L Q K R W I E V F I P R F S I S A S Y N G E T I L P K M G I Q N A E D E N E L T H D I I T K F L E N E D R R S A S L H L P K L S I T G T Y D E K S V L G Q L G E T K V F S
LSI-01 pdb1qlp	K N A D F S G I A K R D S I Q V S K A T H K A V E D V S E E G T E A T A T A T T T K F I V R S K D G P N G A D L S G V T E E A P I K L S K A V H K A V L T I D E K G T E A A G A M F L E A P P M S I . . P
LSI-01 pdb1qlp	S . Y F T V S F N R T F L M M I T N K A T D G I E F L G K V E N P T K S P E . . V K F N K P F V F L M I E Q N T K S P I F M G K V V N P T Q K

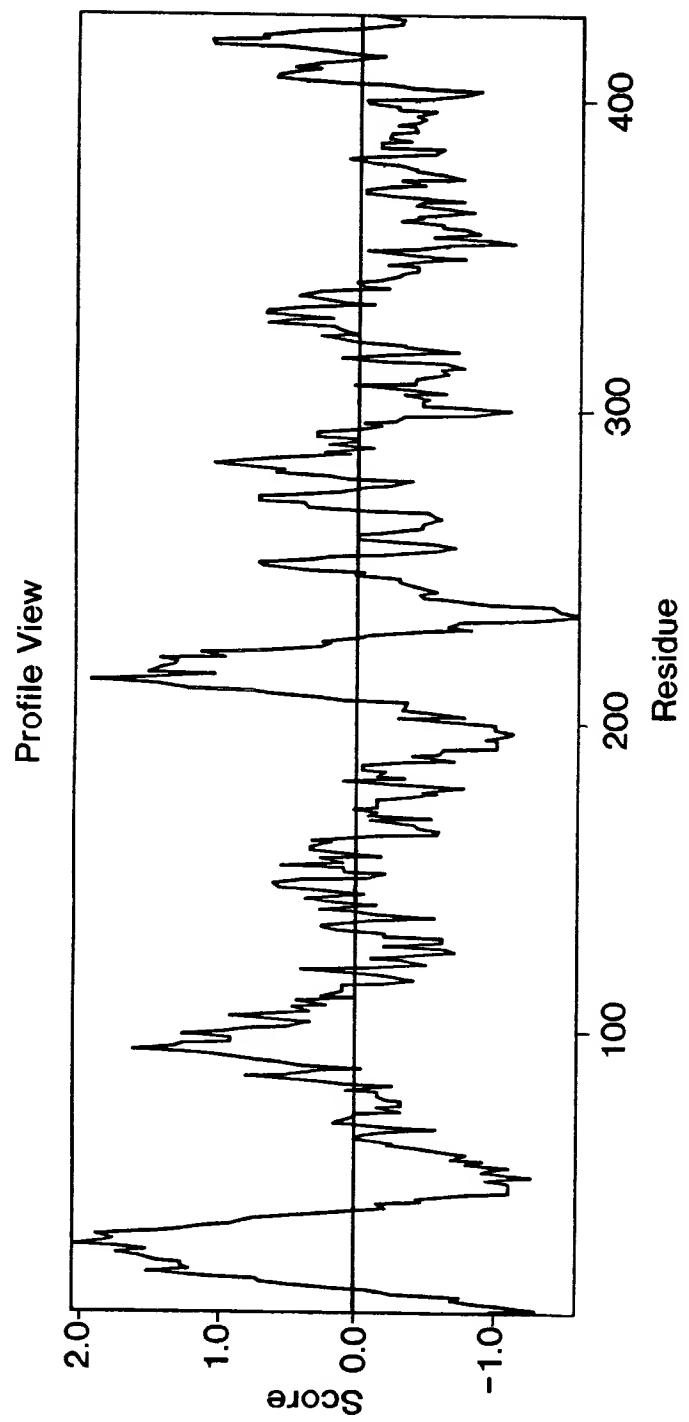


FIG. 4

FIG. 5A

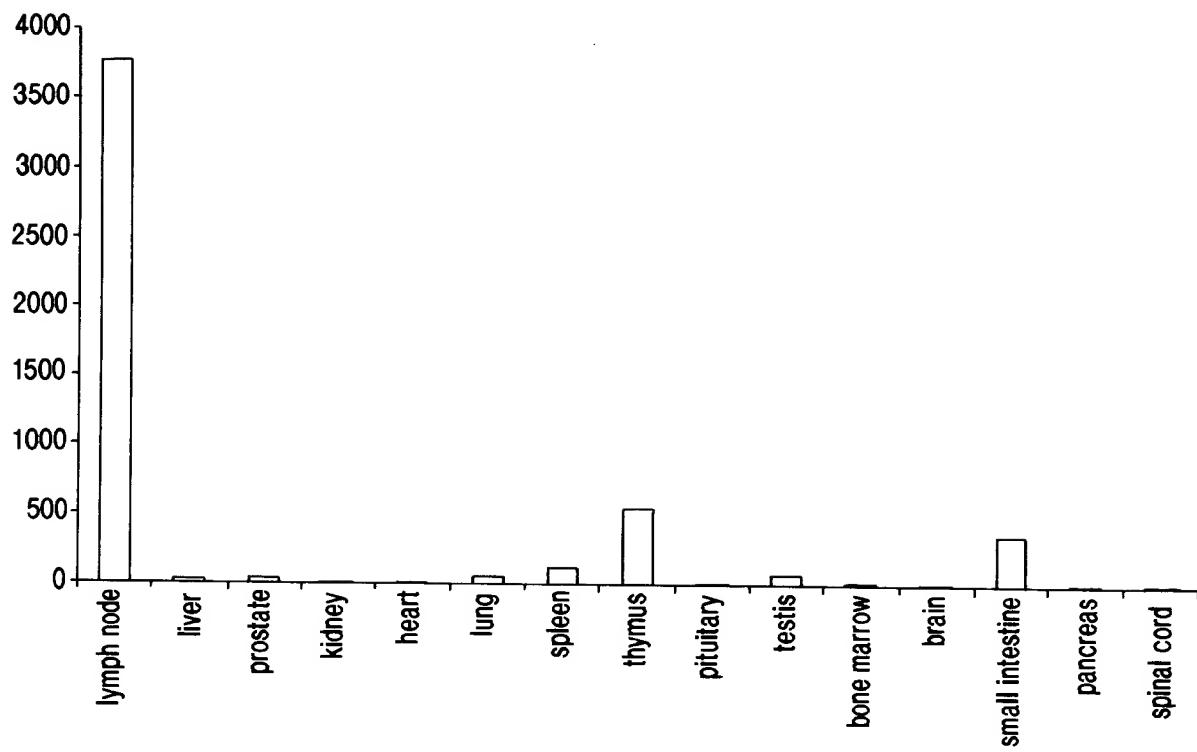


FIG. 5B

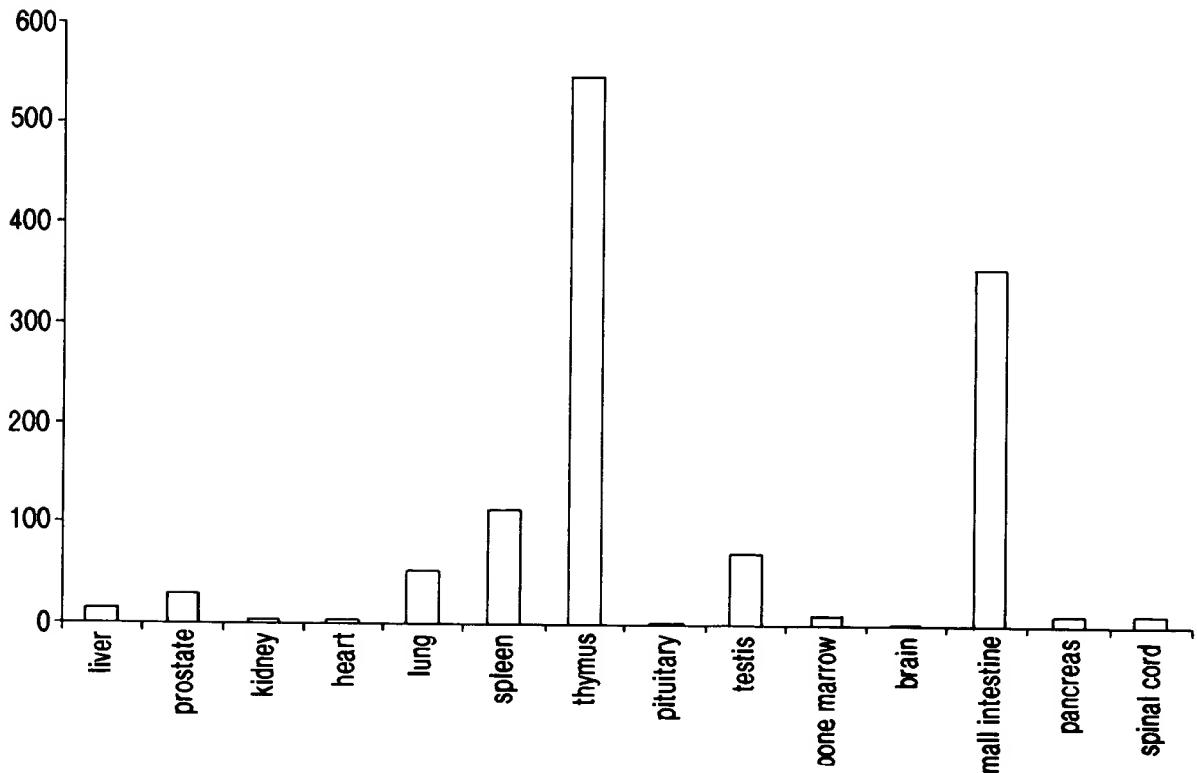


FIG. 6

Protein	Genbank ID	Identities	Similarities
human α_1 -antichymotrypsin	gi 112874	46%	52%
human Kallistatin	gi 5453888	48%	56%
human thyroxin-binding globulin	gi 37142	51%	57%
human α_1 -antitrypsin	gi 6137432	43%	50%

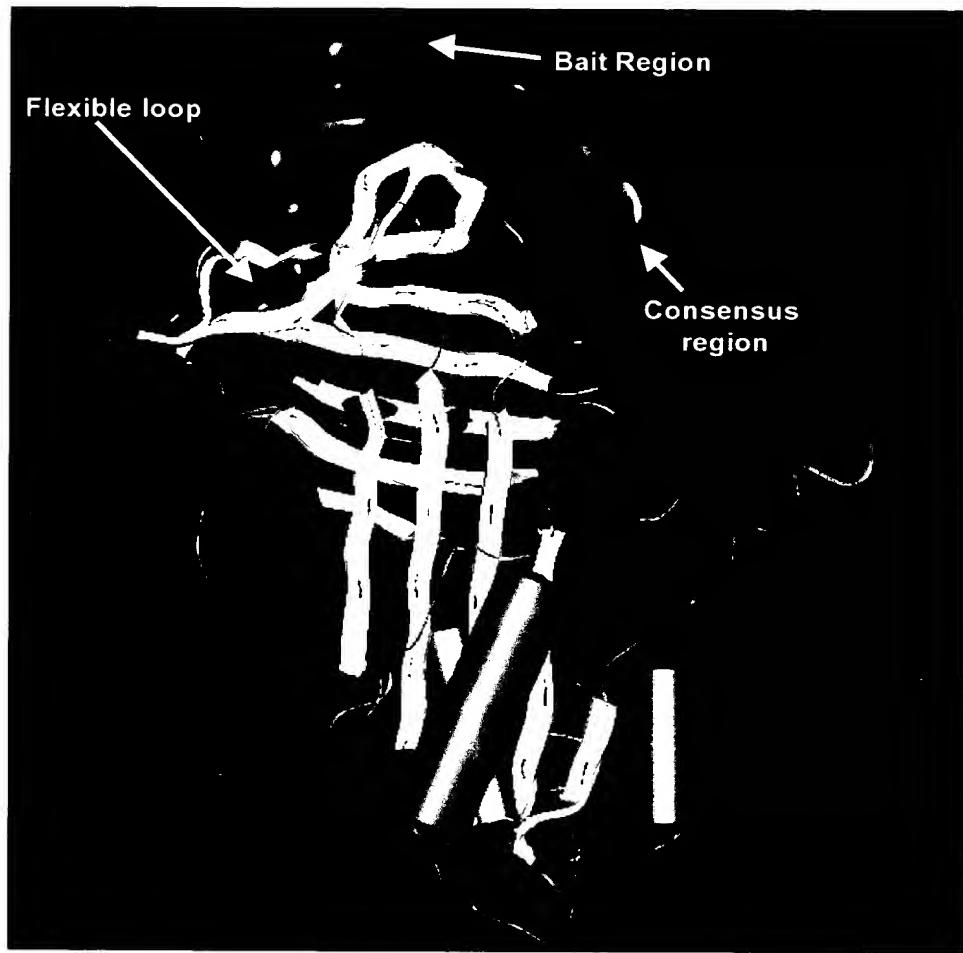


FIG. 7